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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 74220
- (i) APPLICANTS: DiTullio, Paul A.; Meade, Harry; Cole, Edward S.
 - (ii) TITLE OF INVENTION: TRANSGENETICALLY PRODUCED ANTITHROMBIN III
 - (iii) NUMBER OF SEQUENCES: 2
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/391,743
 - (B) FILING DATE: 21-FEB-1995
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Myers, Paul Louis
 - (B) REGISTRATION NUMBER: 35,965
 - (C) REFERENCE/DOCKET NUMBER: TCI-045
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: YES
 - (v) FRAGMENT TYPE: N-terminal
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACAATTTACC CCAAGATCTC AAAGACCCAC TGAATACTAA AGAGACCTCA TTGTGGTTAC	60
AATAATTTGG GGAAGTGGCC AAAACTTCCG TGCATCCCAG CCAAGATCTG TAGCTACTGG	120
ACAATTTTCAT TTCCTTTATC AGATTGTGAG TTATTCTGTG TAAAATGCTC CCCAGAATTT	180
CTGGGGACAG AAAAATAGGA AGAATTCATT TCCTAATCAT GCAGATTTCT AGGAATTCAA	240
ATCCACTGTT GGTTTTATTT CAAACCACAA AATTAGCATG CCATTAAATA CTATATATAA	300
ACAGCCACTA AATCAGATCA TTATCCATTC AGCTTCTCTT TCACTTCTTC TCCTCTACTT	360
TGGAAAAAAG GTAAGAATCT CAGATATAAT TTCAGTGTAT CTGCTACTCA TCTTTATTTT	420
GGACTAGGTT AAAATGTAGA AAGAACATAA TTGCTTAAAA TAGATCTTAA AAATAAGGCT	480
GTTTAAGATA AGCTTTACAC TATTTTCAGC AGATATGTAA AAAAATACAA GTGACTATAA	540
AGACTTGATA AAAATTATAG GTGACTGCAA TTTTGTCCAT GAGGTTTGCA GGATCTTGGT	600
TCCCTGACCA GGGATCAAAC CTGCACTCCC CTGGAAGCAT GGAGTCTTGG ACATTTGTAT	660
TATACACTAT CTTTGGTTCC TTTTAAAGGG AAGTAATTTT ACTTAAATAA GAAAATAGAT	720
TGACAACTAA TACGCTGTTT CCTCATCTTC CCATTCACAG GAATCGAGAG CCATGAAGGT	780
CCTCATCTCT GCCTGTCTGG TGGCTCTGGC CATTTGCAAGA ACAAAGAGGT AAATACAGAA	840
AAAATGTTGA AATAATAGAC TAGTACTGTC TGCCTATGTG TAGAAATCAC ATTACCAACA	900
TCATAAATGT ATAAATAATG CACAATCTCA GATTTATTTT TTAATGCTAA GAAAGTCATT	960
TATGTTTCATC CACTATCTCA ACAGTATCCT ATAGGACCAC AACTCTGGGT CAAGTGCTTT	1020
CTATAGTATT GTACCATCTG TACCATCAAT TCCTAAAGAA AAAGGAAAAG AAACCAATAA	1080
GCAACAGACC AACAAGAAGG AACACAGACA AGAACAAAAA ATGAGTAATA TTGTACAAAT	1140
ACAATTGCAC CCTGCAGGAA CTAAAGTGTT TTTTTTCTC TCTCTTTTCA GCAGGAAGAA	1200
CTCAATGTAG TCGGTGAGGT AAGATGATTT TTATACAAAG AAAAAAATA ATTTAACTGT	1260
AAAATAGTAA CAGACTCTGA TGATCTAGCA GAAAACTCAG CTAATTGTCA ATTTTATTTT	1320
TTCTTTTATA GACTGTGGAA AGCCTTTTCA AGCAGTGAGG TAAGATAATG TTCATTCAGA	1380
GGCAATTTCC CAGATTTAGA GCAATAAAAC ACTGTATTAT CTTTTTGTGT TACATTAATT	1440
GGCAACCCAC TCCAGTACTC TTGACAAATA TGAATTTTTC TTTAAAGCTA AACCTGATTT	1500
TATTTTATTT TTTCCAAAGG AATCTATTAC ACACATCAAT AAGGTAAAAC CTTTATATTT	1560
AAACGTATCA TTTTAAAAA TTTCATGTTT GATTTTATA AACAGCATTT CTTTATGTGT	1620
GATTTTTTTT TTTACCAGAA AATTGAGAAG TTTCAAAGTG AGGAACAACA GCAACAGAG	1680

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GTAATTTGTT TCACTATGAG TATATTTTGA GAAGTATTAT GAAACATAAC ACATAAAAGA	1740
TTTATAATAA TTATGTTTCAG TCTAAGAATG GTAATATAAG TGTCAGTGTA AGAAATGAAA	1800
ACTTTGACAA AATGAAAATA TTTTAAAGAT AGAAACACAT TTTTAAACAC ATAATCAAAAT	1860
TTTACAGTAT AGAATAAATA CCCAAGAATA ACTACTGGTA TATTCATTTT ACTAATGGTA	1920
TACCTGGCTT TAATAAATGC ATATTAGTAG GAACAATTCC AACTAGGGA CTGTGATCCC	1980
CTTATTCTAA TGATGGATAT GCTGATGAAA GACAGTAGGG TGACAGTGTG GCACTAATCC	2040
TAATAAATGG AAGATTTTCT TTCTCTCTCT TCACTGAATT ATGTTTTTAA AAGAGGAGGA	2100
TAATTCATCA TGAATAACAA TTATAACTGG ATTATGGACT GCAAAGGCAT TGGTTTTCTT	2160
TCTTTCCAGG ATGAACATCA GGATAAAATC CACCCCTTTG CCCAGGCACA AAGTCTCTAG	2220
TCTATCCCTT CACTGGGCCC ATCCCTAACA GCCTCCACCA AAACATCCTG CTGCTCTTAC	2280
TCAAACCCCT GTGGTGGTGC CGCCTTTCTT TCAGCTGAA ATAATGGGAG TCCTTGCCAA	2340
AGTGAAGGAG ACTATGGTTC CTAAGCACAA AGAAATGCCC TCCCTAAAT ATCCAGTTG	2400
AGCCCTTTAC TGAAAGCCAG AGCCTGACTC TCACTGATGT TGAAAGCTG CACCTTCTTT	2460
CTCTGCCTCT GGTCCAGTCT TGGATGCACC AGCCTCCCCA GCCTCTTTCT CCAACCGTCA	2520
TTGTTTCCTC CTCAGTCCGT GCTGTCCCTT TCTCAGCCCA AAGTTCTGCC TGTTCGCCAG	2580
AAAGCAGTGC CCCAGAGAGA TATGCCCATC CAGGCCCTTC TGCTGTACCA GGAGCCTGTA	2640
CAATTGGTCC TGTCCGGGGA CCCTTCCCTA TTCTTGTAAG TCTAAATTTA CTAAGTGTGC	2700
TGTGGTTAAC TTCTGATGTT TGTATGATAT TTGAGTAATT AAGAGCCCTA CAAAAAATC	2760
AATAATGAAT GGTTCGAAAA TAAGCATAGC TGAGATTAAT GATTCCTCAGC ATTAGTTATA	2820
AATAGAATAA GCTGGAAAAC CTTACCTCC CCTCCACCAC CAGATCCCA AAACAAAATA	2880
CTGAACATGC TTATTTCAAT ACTCAGGGA AATTTTCTTG CCAAAAAGGC AAGAATTGTA	2940
TAATTCATTC ACTTATTTTA TTTTTTTTAA TTTTAAAGGT CTAAGAGGAT TTCAAAGTGA	3000
ATGCCCCCTC CTCACTTTTC GTCAAATTGG AAATGGGGGT GAGATGAAGA GTTATAACAT	3060
ATAACTAAAT GGACATTTGT CTCTATTCCA CAGAATTGAC TCCGACTGGA AATATGGCAA	3120
CTTTTCAATC CTTGCATCAT GCTACTAAGA TAATTTTAA ATGAGTATAC ATGGGACAAA	3180
AAATGAAACT TTATTCCTTT ATTTATTTTA TGCTTTTTC TCTTAATTG AATTTGAGTC	3240
ATAAACCATA TACTTICAAA ATGTTAATTC AACATTAGCA TAAAAGTTCA ATTTTAACTT	3300
GGAAATATCA TGAACATATC AAATTATGTA TAAAAATAAT TTCTGGAATT GTGATTATTA	3360
TTTCTTTAAG AATCTATTTT CTAACCAGTC ATTTCAATAA ATTAACCCTT AGGCATATTT	3420

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AAGTTTTCCTT GTCTTTATTA TATTTTAAA AATGAAATTG GTCTCTTTAT TGTAACTTA 3480

AATTTATCTT TGATGTTAAA AATAGCTGTG GAAAA 3515

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Leu Ile Leu Ala Cys Leu Val Ala Leu Ala Ile Ala Arg
 1 5 10 15

Glu Gln Glu Glu Leu Asn Val Val Gly Glu Thr Val Glu Ser Leu Ser
 20 25 30

Ser Ser Glu Glu Ser Ile Thr His Ile Asn Lys Lys Ile Glu Lys Phe
 35 40 45

Gln Ser Glu Glu Gln Gln Gln Thr Glu Asp Glu Leu Gln Asp Lys Ile
 50 55 60

His Pro Phe Ala Gln Ala Gln Ser Leu Val Tyr Pro Phe Thr Gly Pro
 65 70 75 80

Ile Pro Asn Ser Leu Pro Gln Asn Ile Leu Pro Leu Thr Gln Thr Pro
 85 90 95

Val Val Val Pro Pro Phe Leu Gln Pro Glu Ile Met Gly Val Pro Lys
 100 105 110

Val Lys Glu Thr Met Val Pro Lys His Lys Glu Met Pro Phe Pro Lys
 115 120 125

Tyr Pro Val Glu Pro Phe Thr Glu Ser Gln Ser Leu Thr Leu Thr Asp
 130 135 140

Val Glu Lys Leu His Leu Pro Leu Pro Leu Val Gln Ser Trp Met His
 145 150 155 160

Gln Pro Pro Gln Pro Leu Ser Pro Thr Val Met Phe Pro Pro Gln Ser
 165 170 175

Val Leu Ser Leu Ser Gln Pro Lys Val Leu Pro Val Pro Gln Lys Ala
 180 185 190

Val Pro Gln Arg Asp Met Pro Ile Gln Ala Phe Leu Leu Tyr Gln Glu
 195 200 205

Pro Val Leu Gly Pro Val Arg Gly Pro Phe Pro Ile Leu Val
 210 215 220

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